

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/263,689DATE: 07/22/1999
TIME: 10:08:40

INPUT SET: S32606.raw

<p>This Raw Listing contains the General Information Section and up to the first 5 pages.</p>

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Ni, Jian
6 Gentz, Reiner L.
7 Ruben, Steven M.
8
9 (ii) TITLE OF INVENTION: Galectin 8, 9, 10 and 10SV
10
11 (iii) NUMBER OF SEQUENCES: 60
12
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Sterne, Kessler, Goldstein, & Fox P.L.L.C.
15 (B) STREET: 1100 New York Ave., Suite 600
16 (C) CITY: Washington
17 (D) STATE: D.C.
18 (E) COUNTRY: USA
19 (F) ZIP: 20005-3934
20
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26
27 (vi) CURRENT APPLICATION DATA:
28 (A) APPLICATION NUMBER: 09/263,689
29 (B) FILING DATE:
30 (C) CLASSIFICATION:
31
32 (vii) PRIOR APPLICATION DATA:
33 (A) APPLICATION NUMBER: 08/946,914
34 (B) FILING DATE:
35
36 (viii) ATTORNEY/AGENT INFORMATION:
37 (A) NAME: Steffe, Eric K.
38 (B) REGISTRATION NUMBER: 36,688
39 (C) REFERENCE/DOCKET NUMBER: 1488.0560001/EKS/SGW
40
41 (ix) TELECOMMUNICATION INFORMATION:
42 (A) TELEPHONE: 202-371-2600
43 (B) TELEFAX: 202-371-2540
44
45
46 (2) INFORMATION FOR SEQ ID NO:1:

ENTERED

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47
48      (i) SEQUENCE CHARACTERISTICS:
49          (A) LENGTH: 1138 base pairs
50          (B) TYPE: nucleic acid
51          (C) STRANDEDNESS: double
52          (D) TOPOLOGY: both
53
54      (ii) MOLECULE TYPE: cDNA
55
56
57      (ix) FEATURE:
58          (A) NAME/KEY: CDS
59          (B) LOCATION: 52..1020
60
61
62      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
63
64      TTCGGCACGA GAGCTCTTCT CACAGGACCA GCCACTAGCG CACCTCGAGC G ATG GCC      57
65                                          Met Ala
66                                          1
67
68      TAT GTC CCC GCA CCG GGC TAC CAG CCC ACC TAC AAC CCG ACG CTG CCT      105
69      Tyr Val Pro Ala Pro Gly Tyr Gln Pro Thr Tyr Asn Pro Thr Leu Pro
70              5              10              15
71
72      TAC TAC CAG CCC ATC CCG GGC GGG CTC AAC GTG GGA ATG TCT GTT TAC      153
73      Tyr Tyr Gln Pro Ile Pro Gly Gly Leu Asn Val Gly Met Ser Val Tyr
74              20              25              30
75
76      ATC CAA GGA GTG GCC AGC GAG CAC ATG AAG CGG TTC TTC GTG AAC TTT      201
77      Ile Gln Gly Val Ala Ser Glu His Met Lys Arg Phe Phe Val Asn Phe
78              35              40              45              50
79
80      GTG GTT GGG CAG GAT CCG GGC TCA GAC GTC GCC TTC CAC TTC AAT CCG      249
81      Val Val Gly Gln Asp Pro Gly Ser Asp Val Ala Phe His Phe Asn Pro
82              55              60              65
83
84      CGG TTT GAC GGC TGG GAC AAG GTG GTC TTC AAC ACG TTG CAG GGC GGG      297
85      Arg Phe Asp Gly Trp Asp Lys Val Val Phe Asn Thr Leu Gln Gly Gly
86              70              75              80
87
88      AAG TGG GGC AGC GAG GAG AGG AAG AGG AGC ATG CCC TTC AAA AAG GGT      345
89      Lys Trp Gly Ser Glu Glu Arg Lys Arg Ser Met Pro Phe Lys Lys Gly
90              85              90              95
91
92      GCC GCC TTT GAG CTG GTC TTC ATA GTC CTG GCT GAG CAC TAC AAG GTG      393
93      Ala Ala Phe Glu Leu Val Phe Ile Val Leu Ala Glu His Tyr Lys Val
94              100              105              110
95
96      GTG GTA AAT GGA AAT CCC TTC TAT GAG TAC GGG CAC CGG CTT CCC CTA      441
97      Val Val Asn Gly Asn Pro Phe Tyr Glu Tyr Gly His Arg Leu Pro Leu
98              115              120              125              130
99

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100	CAG ATG GTC ACC CAC CTG CAA GTG GAT GGG GAT CTG CAA CTT CAA TCA	489
101	Gln Met Val Thr His Leu Gln Val Asp Gly Asp Leu Gln Leu Gln Ser	
102	135 140 145	
103		
104	ATC AAC TTC ATC GGA GGC CAG CCC CTC CGG CCC CAG GGA CCC CCG ATG	537
105	Ile Asn Phe Ile Gly Gly Gln Pro Leu Arg Pro Gln Gly Pro Pro Met	
106	150 155 160	
107		
108	ATG CCA CCT TAC CCT GGT CCC GGA CAT TGC CAT CAA CAG CTG AAC AGC	585
109	Met Pro Pro Tyr Pro Gly Pro Gly His Cys His Gln Gln Leu Asn Ser	
110	165 170 175	
111		
112	CTG CCC ACC ATG GAA GGA CCC CCA ACC TTC AAC CCG CCT GTG CCA TAT	633
113	Leu Pro Thr Met Glu Gly Pro Pro Thr Phe Asn Pro Pro Val Pro Tyr	
114	180 185 190	
115		
116	TTC GGG AGG CTG CAA GGA GGG CTC ACA GCT CGA AGA ACC ATC ATC ATC	681
117	Phe Gly Arg Leu Gln Gly Gly Leu Thr Ala Arg Arg Thr Ile Ile Ile	
118	195 200 205 210	
119		
120	AAG GGC TAT GTG CCT CCC ACA GGC AAG AGC TTT GCT ATC AAC TTC AAG	729
121	Lys Gly Tyr Val Pro Pro Thr Gly Lys Ser Phe Ala Ile Asn Phe Lys	
122	215 220 225	
123		
124	GTG GGC TCC TCA GGG GAC ATA GCT CTG CAC ATT AAT CCC CGC ATG GGC	777
125	Val Gly Ser Ser Gly Asp Ile Ala Leu His Ile Asn Pro Arg Met Gly	
126	230 235 240	
127		
128	AAC GGT ACC GTG GTC CGG AAC AGC CTT CTG AAT GGC TCG TGG GGA TCC	825
129	Asn Gly Thr Val Val Arg Asn Ser Leu Leu Asn Gly Ser Trp Gly Ser	
130	245 250 255	
131		
132	GAG GAG AAG AAG ATC ACC CAC AAC CCA TTT GGT CCC GGA CAG TTC TTT	873
133	Glu Glu Lys Lys Ile Thr His Asn Pro Phe Gly Pro Gly Gln Phe Phe	
134	260 265 270	
135		
136	GAT CTG TCC ATT CGC TGT GGC TTG GAT CGC TTC AAG GTT TAC GCC AAT	921
137	Asp Leu Ser Ile Arg Cys Gly Leu Asp Arg Phe Lys Val Tyr Ala Asn	
138	275 280 285 290	
139		
140	GGC CAG CAC CTC TTT GAC TTT GCC CAT CGC CTC TCG GCC TTC CAG AGG	969
141	Gly Gln His Leu Phe Asp Phe Ala His Arg Leu Ser Ala Phe Gln Arg	
142	295 300 305	
143		
144	GTG GAC ACA TTG GAA ATC CAG GGT GAT GTC ACC TTG TCC TAT GTC CAG	1017
145	Val Asp Thr Leu Glu Ile Gln Gly Asp Val Thr Leu Ser Tyr Val Gln	
146	310 315 320	
147		
148	ATC TAATCTATTC CTGGGGCCAT AACTCATGGG AAAACAGAAT TATCCCCTAG	1070
149	Ile	
150		
151		
152	GACTCCTTTC TAAGCCCCTA ATAAAATGTC TGAGGGTGTC TCATGAAAAA AAAAAAAAAA	1130

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153
154 AAAAAAAAAA 1138
155
156
157 (2) INFORMATION FOR SEQ ID NO:2:
158
159 (i) SEQUENCE CHARACTERISTICS:
160 (A) LENGTH: 323 amino acids
161 (B) TYPE: amino acid
162 (D) TOPOLOGY: linear
163
164 (ii) MOLECULE TYPE: protein
165
166 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
167
168 Met Ala Tyr Val Pro Ala Pro Gly Tyr Gln Pro Thr Tyr Asn Pro Thr
169 1 5 10 15
170
171 Leu Pro Tyr Tyr Gln Pro Ile Pro Gly Gly Leu Asn Val Gly Met Ser
172 20 25 30
173
174 Val Tyr Ile Gln Gly Val Ala Ser Glu His Met Lys Arg Phe Phe Val
175 35 40 45
176
177 Asn Phe Val Val Gly Gln Asp Pro Gly Ser Asp Val Ala Phe His Phe
178 50 55 60
179
180 Asn Pro Arg Phe Asp Gly Trp Asp Lys Val Val Phe Asn Thr Leu Gln
181 65 70 75 80
182
183 Gly Gly Lys Trp Gly Ser Glu Glu Arg Lys Arg Ser Met Pro Phe Lys
184 85 90 95
185
186 Lys Gly Ala Ala Phe Glu Leu Val Phe Ile Val Leu Ala Glu His Tyr
187 100 105 110
188
189 Lys Val Val Val Asn Gly Asn Pro Phe Tyr Glu Tyr Gly His Arg Leu
190 115 120 125
191
192 Pro Leu Gln Met Val Thr His Leu Gln Val Asp Gly Asp Leu Gln Leu
193 130 135 140
194
195 Gln Ser Ile Asn Phe Ile Gly Gly Gln Pro Leu Arg Pro Gln Gly Pro
196 145 150 155 160
197
198 Pro Met Met Pro Pro Tyr Pro Gly Pro Gly His Cys His Gln Gln Leu
199 165 170 175
200
201 Asn Ser Leu Pro Thr Met Glu Gly Pro Pro Thr Phe Asn Pro Pro Val
202 180 185 190
203
204 Pro Tyr Phe Gly Arg Leu Gln Gly Gly Leu Thr Ala Arg Arg Thr Ile
205 195 200 205

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206
207 Ile Ile Lys Gly Tyr Val Pro Pro Thr Gly Lys Ser Phe Ala Ile Asn
208 210 215 220
209
210 Phe Lys Val Gly Ser Ser Gly Asp Ile Ala Leu His Ile Asn Pro Arg
211 225 230 235 240
212
213 Met Gly Asn Gly Thr Val Val Arg Asn Ser Leu Leu Asn Gly Ser Trp
214 245 250 255
215
216 Gly Ser Glu Glu Lys Lys Ile Thr His Asn Pro Phe Gly Pro Gly Gln
217 260 265 270
218
219 Phe Phe Asp Leu Ser Ile Arg Cys Gly Leu Asp Arg Phe Lys Val Tyr
220 275 280 285
221
222 Ala Asn Gly Gln His Leu Phe Asp Phe Ala His Arg Leu Ser Ala Phe
223 290 295 300
224
225 Gln Arg Val Asp Thr Leu Glu Ile Gln Gly Asp Val Thr Leu Ser Tyr
226 305 310 315 320
227
228 Val Gln Ile
229
230

(2) INFORMATION FOR SEQ ID NO:3:

233 (i) SEQUENCE CHARACTERISTICS:
234 (A) LENGTH: 1545 base pairs
235 (B) TYPE: nucleic acid
236 (C) STRANDEDNESS: double
237 (D) TOPOLOGY: both
238

239 (ii) MOLECULE TYPE: cDNA
240
241

242 (ix) FEATURE:
243 (A) NAME/KEY: CDS
244 (B) LOCATION: 16..948
245
246

247 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
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249	AGAGGCGGCG GAGAG ATG GCC TTC AGC GGT TCC CAG GCT CCC TAC CTG AGT	51
250	Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser	
251	1 5 10	
252		
253	CCA GCT GTC CCC TTT TCT GGG ACT ATT CAA GGA GGT CTC CAG GAC GGA	99
254	Pro Ala Val Pro Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly	
255	15 20 25	
256		
257	CTT CAG ATC ACT GTC AAT GGG ACC GTT CTC AGC TCC AGT GGA ACC AGG	147
258	Leu Gln Ile Thr Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg	

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SEQUENCE VERIFICATION REPORT
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Original Text